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SEQUENCE LISTING

<110> Hayward, Nicholas  
Silins, Ginters  
Grimmond, Sean  
Gartside, Michael  
Hancock, John

<120> A NOVEL GENE AND USES THEREFOR

<130> 13198

<140> 09/424,458

<141> 2000-03-16

<150> PCT/AU98/00380

<151> 1998-05-22

<160> 111

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Peptide repeat  
motif in DnaJ homologues.

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160 165 170	

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Ile	Leu	Phe	Gln	Asp	Tyr	His	Ser	Phe	Val	Thr	His	Gly	Cys	Thr	Val	
		175					180					185				
gac	aac	ccc	gtc	ctg	gag	cgg	ttc	atc	tcc	ctc	ttc	aac	agc	gtc	tca	865
Asp	Asn	Pro	Val	Leu	Glu	Arg	Phe	Ile	Ser	Leu	Phe	Asn	Ser	Val	Ser	
	190					195					200					
cag	tgg	gtg	cag	ctc	atg	atc	ctc	agc	aaa	ccc	aca	gcc	ccg	cag	cgg	913
Gln	Trp	Val	Gln	Leu	Met	Ile	Leu	Ser	Lys	Pro	Thr	Ala	Pro	Gln	Arg	
205					210					215					220	
gcc	ctg	gtc	atc	aca	cac	ttt	gtc	cac	gtg	gcg	gag	aag	ctg	cta	cag	961
Ala	Leu	Val	Ile	Thr	His	Phe	Val	His	Val	Ala	Glu	Lys	Leu	Leu	Gln	
				225					230					235		
ctg	cag	aac	ttc	aac	acg	ctg	atg	gca	gtg	gtc	ggg	ggc	ctg	agc	cac	1009
Leu	Gln	Asn	Phe	Asn	Thr	Leu	Met	Ala	Val	Val	Gly	Gly	Leu	Ser	His	
			240					245					250			
agc	tcc	atc	tcc	cgc	ctc	aag	gag	acc	cac	agc	cac	gtt	agc	cct	gag	1057
Ser	Ser	Ile	Ser	Arg	Leu	Lys	Glu	Thr	His	Ser	His	Val	Ser	Pro	Glu	
		255					260					265				
acc	atc	aag	ctc	tgg	gag	ggt	ctc	acg	gaa	cta	gtg	acg	gcg	aca	ggc	1105
Thr	Ile	Lys	Leu	Trp	Glu	Gly	Leu	Thr	Glu	Leu	Val	Thr	Ala	Thr	Gly	
	270					275					280					
aac	tat	ggc	aac	tac	cgg	cgt	cgg	ctg	gca	gcc	tgt	gtg	ggc	ttc	cgc	1153
Asn	Tyr	Gly	Asn	Tyr	Arg	Arg	Arg	Leu	Ala	Ala	Cys	Val	Gly	Phe	Arg	
285					290					295					300	
ttc	ccg	atc	ctg	ggt	gtg	cac	ctc	aag	gac	ctg	gtg	gcc	ctg	cag	ctg	1201
Phe	Pro	Ile	Leu	Gly	Val	His	Leu	Lys	Asp	Leu	Val	Ala	Leu	Gln	Leu	
				305					310					315		
gca	ctg	cct	gac	tgg	ctg	gac	cca	gcc	cgg	acc	cgg	ctc	aac	ggg	gcc	1249
Ala	Leu	Pro	Asp	Trp	Leu	Asp	Pro	Ala	Arg	Thr	Arg	Leu	Asn	Gly	Ala	
			320					325					330			
aag	atg	aag	cag	ctc	ttt	agc	atc	ctg	gag	gag	ctg	gcc	atg	gtg	acc	1297
Lys	Met	Lys	Gln	Leu	Phe	Ser	Ile	Leu	Glu	Glu	Leu	Ala	Met	Val	Thr	
		335					340					345				

agc	ctg	cgg	cca	cca	gta	cag	gcc	aac	ccc	gac	ctg	ctg	agc	ctg	ctc	1345
Ser	Leu	Arg	Pro	Pro	Val	Gln	Ala	Asn	Pro	Asp	Leu	Leu	Ser	Leu	Leu	
	350					355					360					
acg	gtg	tct	ctg	gat	cag	tat	cag	acg	gag	gat	gag	ctg	tac	cag	ctg	1393
Thr	Val	Ser	Leu	Asp	Gln	Tyr	Gln	Thr	Glu	Asp	Glu	Leu	Tyr	Gln	Leu	
365					370					375					380	
tcc	ctg	cag	cgg	gag	ccg	cgc	tcc	aag	tcc	tcg	cca	acc	agc	ccc	acg	1441
Ser	Leu	Gln	Arg	Glu	Pro	Arg	Ser	Lys	Ser	Ser	Pro	Thr	Ser	Pro	Thr	
				385					390					395		
agt	tgc	acc	cca	cca	ccc	cgg	ccc	ccg	gta	ctg	gag	gag	tgg	acc	tcg	1489
Ser	Cys	Thr	Pro	Pro	Pro	Arg	Pro	Pro	Val	Leu	Glu	Glu	Trp	Thr	Ser	
			400					405					410			
gct	gcc	aaa	ccc	aag	ctg	gat	cag	gcc	ctc	gtg	gtg	gag	cac	atc	gag	1537
Ala	Ala	Lys	Pro	Lys	Leu	Asp	Gln	Ala	Leu	Val	Val	Glu	His	Ile	Glu	
		415					420					425				
aag	atg	gtg	gag	tct	gtg	ttc	cgg	aac	ttt	gac	gtc	gat	ggg	gat	ggc	1585
Lys	Met	Val	Glu	Ser	Val	Phe	Arg	Asn	Phe	Asp	Val	Asp	Gly	Asp	Gly	
	430					435					440					
cac	atc	tca	cag	gaa	gaa	ttc	cag	atc	atc	cgt	ggg	aac	ttc	cct	tac	1633
His	Ile	Ser	Gln	Glu	Glu	Phe	Gln	Ile	Ile	Arg	Gly	Asn	Phe	Pro	Tyr	
445					450					455					460	
ctc	agc	gcc	ttt	ggg	gac	ctc	gac	cag	aac	cag	gat	ggc	tgc	atc	agc	1681
Leu	Ser	Ala	Phe	Gly	Asp	Leu	Asp	Gln	Asn	Gln	Asp	Gly	Cys	Ile	Ser	
				465					470					475		
agg	gag	gag	atg	gtt	tcc	tat	ttc	ctg	cgc	tcc	agc	tct	gtg	ttg	ggg	1729
Arg	Glu	Glu	Met	Val	Ser	Tyr	Phe	Leu	Arg	Ser	Ser	Ser	Val	Leu	Gly	
			480					485					490			
ggg	cgc	atg	ggc	ttc	gta	cac	aac	ttc	cag	gag	agc	aac	tcc	ttg	cgc	1777
Gly	Arg	Met	Gly	Phe	Val	His	Asn	Phe	Gln	Glu	Ser	Asn	Ser	Leu	Arg	
		495					500					505				
ccc	gtc	gcc	tgc	cgc	cac	tgc	aaa	gcc	ctg	atc	ctg	ggc	atc	tac	aag	1825
Pro	Val	Ala	Cys	Arg	His	Cys	Lys	Ala	Leu	Ile	Leu	Gly	Ile	Tyr	Lys	
	510					515					520					

cag ggc ctc aaa tgc cga gcc tgt gga gtg aac tgc cac aag cag tgc 1873  
 Gln Gly Leu Lys Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys  
 525 530 535 540  
 aag gat cgc ctg tca gtt gag tgt cgg cgc agg gcc cag agt gtg agc 1921  
 Lys Asp Arg Leu Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser  
 545 550 555  
 ctg gag ggg tct gca ccc tca ccc tca ccc atg cac agc cac cat cac 1969  
 Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His Ser His His His  
 560 565 570  
 cgc gcc ttc agc ttc tct ctg ccc cgc cct ggc agg cga ggc tcc agg 2017  
 Arg Ala Phe Ser Phe Ser Leu Pro Arg Pro Gly Arg Arg Gly Ser Arg  
 575 580 585  
 cct cca gag atc cgt gag gag gag gta cag acg gtg gag gat ggg gtg 2065  
 Pro Pro Glu Ile Arg Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val  
 590 595 600  
 ttt gac atc cac ttg taatagatgc tgtggttgga tcaaggactc attcctgcct 2120  
 Phe Asp Ile His Leu  
 605  
 tggagaaaat acttcaacca gagcagggag cctgggggtg tcggggcagg aggctgggga 2180  
 tgggggtggg atatgagggg ggcattgcagc tgagggcagg gccagggctg gtgtccctaa 2240  
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 ttaaccttc 2309

<210> 7  
 <211> 609  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu  
 1 5 10 15  
 Leu Arg Gly Cys Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp  
 20 25 30



17

Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro  
 340 345 350  
 Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu  
 355 360 365  
 Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg  
 370 375 380  
 Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro  
 385 390 395 400  
 Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser Ala Ala Lys Pro  
 405 410 415  
 Lys Leu Asp Gln Ala Leu Val Val Glu His Ile Glu Lys Met Val Glu  
 420 425 430  
 Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln  
 435 440 445  
 Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe  
 450 455 460  
 Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met  
 465 470 475 480  
 Val Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly  
 485 490 495  
 Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys  
 500 505 510  
 Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys  
 515 520 525  
 Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu  
 530 535 540  
 Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser  
 545 550 555 560  
 Ala Pro Ser Pro Ser Pro Met His Ser His His His Arg Ala Phe Ser  
 565 570 575  
 Phe Ser Leu Pro Arg Pro Gly Arg Arg Gly Ser Arg Pro Pro Glu Ile  
 580 585 590  
 Arg Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val Phe Asp Ile His  
 595 600 605  
 Leu

<210> 8  
 <211> 832  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (11)..(733)

<400> 8  
 gccgcgccgccc atg ccg ccc tta ctg ccc ctg cgc ctg tgc cgg ctg tgg 49  
 Met Pro Pro Leu Leu Pro Leu Arg Leu Cys Arg Leu Trp  
 1 5 10  
 ccc cgc aac cct ccc tcc cgg ctc ctc gga gcg gcc gcc ggg cag cgg 97  
 Pro Arg Asn Pro Pro Ser Arg Leu Leu Gly Ala Ala Ala Gly Gln Arg  
 15 20 25  
 tcc aga ccc agt act tat tat gaa ctg ttg ggg gtg cat cct ggt gcc 145  
 Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala  
 30 35 40 45  
 agc act gag gaa gtt aaa cga gct ttc ttc tcc aag tcc aaa gag ctg 193  
 Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu  
 50 55 60  
 cac cca gac cgg gac cct ggg aac cca agc ctg cac agc cgc ttt gtg 241  
 His Pro Asp Arg Asp Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val  
 65 70 75  
 gag ctg agc gag gca tac cgt gtg ctc agc cgt gag cag agc cgc cgc 289  
 Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg  
 80 85 90  
 agc tat gat gac cag ctc cgc tca ggt agt ccc cca aag tct cca cga 337  
 Ser Tyr Asp Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg  
 95 100 105  
 acc aca gtc cat gac aag tct gcc cac caa aca cac agc tcc tgg aca 385  
 Thr Thr Val His Asp Lys Ser Ala His Gln Thr His Ser Ser Trp Thr  
 110 115 120 125  
 ccc ccc aac gca cag tac tgg tcc cag ttt cac agc gtg agg cca cag 433  
 Pro Pro Asn Ala Gln Tyr Trp Ser Gln Phe His Ser Val Arg Pro Gln  
 130 135 140

ggg ccc cag ttg agg cag cag caa cac aaa caa aac aaa caa gtg ctg 481  
 Gly Pro Gln Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val Leu  
 145 150 155  
 ggg tac tgc ctc ctc ctc atg ctg gcg ggc atg ggc ctg cac tac att 529  
 Gly Tyr Cys Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile  
 160 165 170  
 gcc ttc agg aag gtg aag cag atg cac ctt aac ttc atg gat gaa aag 577  
 Ala Phe Arg Lys Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys  
 175 180 185  
 gat cgg atc atc aca gcc ttc tac aac gaa gcc cgg gca cgg gcc agg 625  
 Asp Arg Ile Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg  
 190 195 200 205  
 gcc aac aga ggc atc ctt cag cag gag cga caa cgg cta ggg cag cgg 673  
 Ala Asn Arg Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg  
 210 215 220  
 cag ccg cca cca tcc gag cca acc caa ggc ccc gag atc gtg ccc cgg 721  
 Gln Pro Pro Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val Pro Arg  
 225 230 235  
 ggc gcc ggc ccc tgaggggctc acctggatgg ggctgcagt gcgttcccgc 773  
 Gly Ala Gly Pro  
 240  
 tttgcttctt tccctggacg gcccgctccc cgaaacgcgc gcaataaagt gattcgcag 832

<210> 9  
 <211> 241  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Met Pro Pro Leu Leu Pro Leu Arg Leu Cys Arg Leu Trp Pro Arg Asn  
 1 5 10 15  
 Pro Pro Ser Arg Leu Leu Gly Ala Ala Ala Gly Gln Arg Ser Arg Pro  
 20 25 30  
 Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu  
 35 40 45  
 Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp  
 50 55 60

Arg Asp Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val Glu Leu Ser  
 65 70 75 80  
 Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg Ser Tyr Asp  
 85 90 95  
 Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg Thr Thr Val  
 100 105 110  
 His Asp Lys Ser Ala His Gln Thr His Ser Ser Trp Thr Pro Pro Asn  
 115 120 125  
 Ala Gln Tyr Trp Ser Gln Phe His Ser Val Arg Pro Gln Gly Pro Gln  
 130 135 140  
 Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val Leu Gly Tyr Cys  
 145 150 155 160  
 Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile Ala Phe Arg  
 165 170 175  
 Lys Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile  
 180 185 190  
 Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg Ala Asn Arg  
 195 200 205  
 Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg Gln Pro Pro  
 210 215 220  
 Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val Pro Arg Gly Ala Gly  
 225 230 235 240

Pro

<210> 10  
 <211> 13  
 <212> PRT  
 <213> C. elegans

<400> 10  
 Asp Val Asp Glu Glu Asp Glu Val Glu Asp Ile Glu Phe  
 1 5 10

<210> 11  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Asp Val Asp Gly Asp Gly His Ile Ser Gln Glu Glu Phe  
 1 5 10

<210> 12  
 <211> 13  
 <212> PRT  
 <213> C. elegans

<400> 12  
 Asp His Asp Arg Asp Gly Phe Ile Ser Gln Glu Glu Phe  
   1                  5                  10

<210> 13  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 13  
 Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met  
   1                  5                  10

<210> 14  
 <211> 13  
 <212> PRT  
 <213> C. elegans

<400> 14  
 Asp Val Asp Met Asp Gly Gln Ile Ser Lys Asp Glu Leu  
   1                  5                  10

<210> 15  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe Asn  
   1                  5                  10                  15

Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser Arg  
                   20                  25                  30

Leu Lys Glu Thr His  
                   35

<210> 16  
 <211> 37  
 <212> PRT  
 <213> C. elegans

<400> 16  
 Lys Phe Val His Val Ala Lys His Leu Arg Lys Ile Asn Asn Phe Asn  
   1                  5                  10                  15

Thr Leu Met Ser Val Val Gly Gly Ile Thr His Ser Ser Val Ala Arg  
20 25 30

Leu Ala Lys Thr Tyr  
35

<210> 17  
<211> 50  
<212> PRT  
<213> Homo sapiens

<400> 17  
His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys Arg His  
1 5 10 15

Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg  
20 25 30

Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu Ser Val  
35 40 45

Glu Cys  
50

<210> 18  
<211> 50  
<212> PRT  
<213> C. elegans

<400> 18  
His Asn Phe His Glu Thr Thr Phe Leu Thr Pro Thr Thr Cys Asn His  
1 5 10 15

Cys Asn Lys Leu Leu Trp Gly Ile Leu Arg Gln Gly Phe Lys Cys Lys  
20 25 30

Asp Cys Gly Leu Ala Val His Ser Cys Cys Lys Ser Asn Ala Val Ala  
35 40 45

Glu Cys  
50

<210> 19  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Nucleotide  
sequence of pGEX and mcg7 junction.

<400> 19

gggatcccc tggtc 15

<210> 20  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Nucleotide  
sequence of pGEX and mcg7 junction.

<400> 20  
gaattcggca cgagccgacg g 21

<210> 21  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Nucleotide  
sequence of myc-tag/mcg7 junction.

<400> 21  
atggagcaga agctgatctc cgaggaggac ctgcccgggg cagctggatc cgcagcccac 60  
cccgcgccgg cggccatg 78

<210> 22  
<211> 26  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:The amino acid  
sequence encoded by the nucleotide sequence of SEQ  
ID NO: 21.

<400> 22  
Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Pro Gly Ala Ala Gly  
1 5 10 15  
Ser Ala Ala His Pro Ala Pro Ala Ala Met  
20 25

<210> 23  
<211> 33  
<212> DNA  
<213> Artificial Sequence



<220>  
 <223> Description of Artificial Sequence:Nucleotide  
 sequence of pGEX and mcg7 junction.

<400> 23  
 ggatccgcag cccaccccgcc gccggcggcc atg 33

<210> 24  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:The amino acid  
 sequence encoded by the nucleotide sequence of SEQ  
 ID NO: 23.

<400> 24  
 Gly Ser Ala Ala His Pro Ala Pro Ala Ala Met  
           1                          5                          10

<210> 25  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-7 specific  
 oligonucleotide.

<400> 25  
 ggacaaagtg tgtgatgaac c 21

<210> 26  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-7 specific  
 oligonucleotide.

<400> 26  
 ctcacacctcc gtctgatact g 21

<210> 27  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 27  
 gtagatgtgg atcagcttgg 20

<210> 28  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 28  
 aggtggagaa tgggtcaagg 19

<210> 29  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 29  
 gtcatagtct gtctcctact 20

<210> 30  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 30  
 acatagacag cgtgcctacc 20

<210> 31  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 31  
 tacaacctta gggacaccag 20

<210> 32  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 32  
 tgctgagcct gctcacggtg 20

<210> 33  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 33  
 caagtgaaca gcacgtcc 18

<210> 34  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide

<400> 34  
 gactatctca aggaccagct g 21

<210> 35  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 35  
 ggttcgggtcc gagcccgg 18

<210> 36  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 36  
 ggagcgatac tccaagtagg t 21

<210> 37  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 37  
 agcggggccag gccccttc 18

<210> 38  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 38  
 catcctggtc caatgcgctc 20

<210> 39  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 39  
 gcactgagga agttaaacga gc 22

<210> 40  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 40  
 gctcgtttaa cttcctcagt gc 22

<210> 41  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 41  
 gctcagctcc acaaagcggc t 21

<210> 42  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.

<400> 42  
 accagctccg ctcaggtag 19

<210> 43  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.  
 <400> 43  
 tccaggagct gtgtgttttg 20

<210> 44  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.  
 <400> 44  
 ccagtttcac agcgtgagg 19

<210> 45  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mcg-18 specific  
 oligonucleotide.  
 <400> 45  
 cagcatgagg aggaggcag 19

<210> 46  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys  
 1 5 10 15  
 Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His  
 20 25 30  
 Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp  
 35 40 45  
 Tyr Asn Pro Asn Cys Arg Leu Cys Asn Ile Pro Leu  
 50 55 60

<210> 47  
 <211> 60  
 <212> PRT  
 <213> Mus musculus

<400> 47  
 Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys  
   1                  5                  10                  15  
 Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His  
                   20                  25                  30  
 Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp  
                   35                  40                  45  
 Tyr Asn Pro Asn Cys Arg Leu Cys Asn Thr Pro Leu  
       50                  55                  60

<210> 48  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
 Pro Lys Arg Lys Val Thr Asn Leu Phe Cys Phe Glu His Arg Val Asn  
   1                  5                  10                  15  
 Val Cys Glu His Cys Leu Val Ala Asn His Ala Lys Cys Ile Val Gln  
                   20                  25                  30  
 Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn Pro Asn Cys Arg  
                   35                  40                  45  
 Leu Cys Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys  
       50                  55                  60  
 Tyr Asp Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu  
       65                  70                  75                  80  
 Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly  
                   85                  90                  95  
 Pro Ile Phe Pro Pro Asn Gln  
                   100

<210> 49  
 <211> 103  
 <212> PRT  
 <213> C. elegans

<220>  
 <221> UNSURE  
 <222> (10)  
 <223> Xaa at position 10 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (21)  
 <223> Xaa at position 21 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (55)  
 <223> Xaa at position 55 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (77)  
 <223> Xaa at position 77 can be any amino acid.

<220>  
 <221> UNSURE  
 <222> (87)  
 <223> Xaa at position 87 can be any amino acid.

<400> 49  
 Pro Lys Arg Lys Val Thr Asn Leu Phe Xaa Tyr Glu His Arg Val Asn  
   1                  5                  10                  15  
 Val Cys Glu Leu Xaa Leu Val Asp Asn His Pro Asn Cys Val Val Gln  
                   20                  25                  30  
 Ser Tyr Leu Thr Trp Leu Thr Asp Gln Asp Tyr Asp Pro Asn Cys Ser  
           35                  40                  45  
 Leu Cys Lys Thr Thr Leu Xaa Glu Gly Asp Thr Ile Arg Leu Asn Cys  
   50                  55                  60  
 Leu His Leu Leu His Trp Lys Cys Phe Asp Glu Trp Xaa Gly Asn Phe  
   65                  70                  75                  80  
 Pro Asp Thr Thr Ala Pro Xaa Gly Tyr Arg Cys Pro Cys Cys Ser Gln  
                   85                  90                  95  
 Glu Val Phe Pro Pro Asp Gln  
                   100

<210> 50  
 <211> 45  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Cys Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys Tyr  
   1                  5                  10                  15  
 Asp Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro  
           20                  25                  30



Arg Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys  
                   35                                  40                                  45

<210> 51  
 <211> 45  
 <212> PRT  
 <213> C. elegans

<400> 51  
 Cys Ser Ile Cys Leu Glu Asn Lys Asn Pro Ser Ala Leu Phe Cys Gly  
       1                                  5                                  10                                  15

His Leu Phe Cys Trp Thr Cys Ile Gln Glu His Ala Val Ala Ala Thr  
                                   20                                  25                                  30

Ser Ser Ala Ser Thr Ser Ser Ala Arg Cys Pro Gln Cys  
                   35                                  40                                  45

<210> 52  
 <211> 24  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn  
       1                                  5                                  10                                  15

Pro Asn Cys Arg Leu Cys Asn Ile  
                                   20

<210> 53  
 <211> 24  
 <212> PRT  
 <213> Saccharomyces pombe

<400> 53  
 Cys Ala Thr Thr Asn Thr Pro Lys Trp Arg Arg Asp Glu Ser Gly Asn  
       1                                  5                                  10                                  15

Pro Ile Cys Asn Ala Cys Gly Leu  
                                   20

<210> 54  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
 Ser Ser Thr Pro Gly Pro Glu Glu Val Asp Ser Ala Ser Ala Ala Pro  
       1                                  5                                  10                                  15

Ala Phe Tyr Ser Gln Ala Pro Arg Pro Pro Ala Ser Pro Gly Arg Pro  
 20 25 30

Glu Gln His Thr Val Ile His Met Gly Asn Pro Glu Pro Leu Thr His  
 35 40 45

Ala Pro Arg Lys Val Tyr Asp Thr Arg Asp Asp Asp Arg Thr Pro Gly  
 50 55 60

Leu His  
 65

<210> 55  
 <211> 66  
 <212> PRT  
 <213> Saccharomyces pombe

<400> 55  
 Ala Ser Leu Leu Asn Pro Glu Glu Pro Pro Ser Asn Ser Asp Lys Gln  
 1 5 10 15

Pro Ser Met Ser Asn Gly Pro Lys Ser Glu Val Ser Pro Ser Gln Ser  
 20 25 30

Gln Gln Ala Pro Leu Ile Gln Ser Ser Thr Ser Pro Val Ser Leu Gln  
 35 40 45

Phe Pro Pro Glu Val Gln Gly Ser Asn Val Asp Lys Arg Asn Tyr Ala  
 50 55 60

Leu Asn  
 65

<210> 56  
 <211> 259  
 <212> DNA  
 <213> Homo sapiens

<400> 56  
 ggcctccctc tgatcgatga ggtggtgagc ccagagcccg agcccctcaa cacgtctgac 60  
 ttctctgact ggtctagttt taatgccagc agtaccctg gaccagagga ggtagacagc 120  
 gcctctgctg cccagcctt ctacagccag gcccccggc cccagcttc cccaggccgg 180  
 cccgagcagc acacagtgat ccacatgggc aatcctgagc ccttgactca cgcccctagg 240  
 aaggtgtatg atacgcggg 259

<210> 57  
 <211> 259

<212> DNA  
<213> Homo sapiens

<400> 57  
gggctccctc tgatcgatga ggtgataagc ccagagcccg agcccctcaa ttcctcagac 60  
ttctctgatt ggtccagctt taatgccacc accacctctg tgcaagagga gagagccagc 120  
actccatctg cacctgcttt ctatagccag gctccccgcc ctctccctc cccaagccgt 180  
cccgagcagc acacagtcac acacatgggg agtactgaag ccctggcaca cgcccgaagg 240  
aaagtatatg acacaccgg 259

<210> 58  
<211> 55  
<212> DNA  
<213> Homo sapiens

<400> 58  
gcactgagag agaagctggc cacagtcaac tgggcccggg caggactggg cctcc 55

<210> 59  
<211> 55  
<212> DNA  
<213> Homo sapiens

<400> 59  
gcactgagag aaaagctagc cacagtcaac ttggccccggg caggactggg ctccc 55

<210> 60  
<211> 44  
<212> DNA  
<213> Homo sapiens

<400> 60  
gccttggggtt ggctggcccc gctgctaagg agccgggctg ggtc 44

<210> 61  
<211> 44  
<212> DNA  
<213> Homo sapiens

<400> 61  
gctctggggtt ggctggcccc gctgctcagg agccgggctg ggtc 44

<210> 62  
 <211> 35  
 <212> DNA  
 <213> Homo sapiens

<400> 62  
 ggagactgtg acgatgacaa gtaccgacgt cggcc 35

<210> 63  
 <211> 35  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 ggagactgtg atgatgacaa ataccgccgc cggcc 35

<210> 64  
 <211> 32  
 <212> DNA  
 <213> Homo sapiens

<400> 64  
 cgggatgatg accggacacc aggcctccat gg 32

<210> 65  
 <211> 32  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
 cgggatgatg accggacagc aggcattcat gg 32

<210> 66  
 <211> 190  
 <212> DNA  
 <213> Homo sapiens

<400> 66  
 cgtctgactt ctctgactgg tctagtttta atgccagcag tacccttgga ccagaggagg 60  
 tagacagcgc ctctgctgcc ccagccttct acagccaggc cccccggccc ccagcttccc 120  
 caggccggcc cgagcagcac acagtgatcc acatgggcaa tctgagccc ttgactcacg 180  
 cccctaggaa 190

<210> 67  
<211> 190  
<212> DNA  
<213> Homo sapiens

<400> 67  
cctcagactt ctctgattgg tccagcttta atgccaccac cacctctgtg caagaggaga 60  
gagccagcac tccatctgcg cctgctttct atagccaggc tccccgccct cctccctccc 120  
caagccgtcc cgagcagcac acagtcatac acatggggag tactgaagcc ctggcacacg 180  
ccccaaggaa 190

<210> 68  
<211> 98  
<212> DNA  
<213> Homo sapiens

<400> 68  
gcactgagag agaagctggc cacagtcaac tgggcccggg caggactggg cctccctctg 60  
atcgatgagg tggtagagccc agagcccgag cccctcaa 98

<210> 69  
<211> 98  
<212> DNA  
<213> Homo sapiens

<400> 69  
gcactgagag acaagctagc cacagtcaac tgggcccggg caggactggg cctccctctg 60  
atcgatgagg tgataagccc agagcccgag cccctcaa 98

<210> 70  
<211> 60  
<212> DNA  
<213> Homo sapiens

<400> 70  
gggatgatga ccggacacca ggcctccatg gagactgtga cgatgacaag taccgacgtc 60

<210> 71  
<211> 60  
<212> DNA  
<213> Homo sapiens

<400> 71

ggattgatga ccggacagca ggcattcatg gagactgtga tgatgacaaa taccgccgcc 60

<210> 72  
<211> 75  
<212> DNA  
<213> Homo sapiens

<400> 72  
taccgccctt cggaaccagt gcagcggccg atcagtaaac acagagactg gggatcgatc 60  
atggggcttt gtaag 75

<210> 73  
<211> 74  
<212> DNA  
<213> Mus musculus

<400> 73  
cttccgcgct ttctattacc gtacgcaccg gtcacgatcg gcatcgcgga ggatcgggtca 60  
tgggactttg caag 74

<210> 74  
<211> 85  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Zinc finger  
consensus.

<220>  
<221> UNSURE  
<222> (2)..(3)  
<223> Xaa at position 2 and 3 can be any amino acid.

<220>  
<221> UNSURE  
<222> (5)..(8)  
<223> Xaa at position 5, 6, 7 and 8 can be any amino  
acid.

<220>  
<221> UNSURE  
<222> (10)..(11)  
<223> Xaa at postion 10 and 11 can be any amino acid.

<220>  
<221> UNSURE  
<222> (13)..(16)

<223> Xaa at position 13, 14, 15 and 16 can be any amino acid.

<220>

<221> UNSURE

<222> (18)..(37)

<223> Xaa at position 18-37 can be any amino acid.

<220>

<221> UNSURE

<222> (39)..(40)

<223> Xaa at position 39 and 40 can be any amino acid.

<220>

<221> UNSURE

<222> (42)..(59)

<223> Xaa at position 42-59 can be any amino acid.

<220>

<221> UNSURE

<222> (61)..(62)

<223> Xaa at position 61 and 62 can be any amino acid.

<220>

<221> UNSURE

<222> (64)..(81)

<223> Xaa at position 64-81 can be any amino acid.

<220>

<221> UNSURE

<222> (83)..(84)

<223> Xaa at position 83 and 84 can be any amino acid.

<400> 74

Cys	Xaa	Xaa	His	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa
1				5				10						15	

His	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30	

Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			35					40					45		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	His	Xaa	Xaa	Cys	Xaa
			50				55				60				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			65				70				75				80

Xaa	Cys	Xaa	Xaa	Cys
				85

<210> 75

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Leucine zipper  
finger consensus.

<220>

<221> UNSURE

<222> (2)..(7)

<223> Xaa at position 2-7 can be any amino acid.

<220>

<221> UNSURE

<222> (9)..(14)

<223> Xaa at position 9-14 can be any amino acid.

<220>

<221> UNSURE

<222> (16)..(21)

<223> Xaa at position 16-21 can be any amino acid.

<220>

<221> UNSURE

<222> (23)..(28)

<223> Xaa at position 23-28 can be any amino acid.

<400> 75

Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa
1				5				10						15	

Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu
			20					25				

<210> 76

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Novel leucine  
zipper finger consensus.

<220>

<221> UNSURE

<222> (2)..(7)

<223> Xaa at position 2-7 can be any amino acid.

<220>

<221> UNSURE

<222> (9)

<223> Xaa at position 9 can be any amino acid.

<220>

<221> UNSURE

<222> (11)..(16)



<223> Xaa at position 11-16 can be any amino acid.

<220>

<221> UNSURE

<222> (18)

<223> Xaa at position 18 can be any amino acid.

<220>

<221> UNSURE

<222> (20)..(25)

<223> Xaa at position 20-25 can be any amino acid.

<400> 76

Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu  
20 25

<210> 77

<211> 627

<212> PRT

<213> C. elegans

<400> 77

Met Ser Ser Lys Val Glu Glu Asp Gln His Gln Glu Leu Leu Thr Glu  
1 5 10 15

Asp Gln Leu Val Ala Arg Cys Val Glu Cys Phe Asp Val Asp Glu Glu  
20 25 30

Asp Glu Val Glu Asp Ile Glu Phe Val Asp Ala Leu Phe Leu Ser His  
35 40 45

Gln Trp Leu Ser Asp Ser Leu Ser Leu Ile Thr His Phe Val Asn Phe  
50 55 60

Tyr Gln Glu Thr Arg Asn Val Glu Gln Arg Glu Ala Val Cys Arg Ala  
65 70 75 80

Val Ser Phe Trp Ile Glu Lys Phe Pro Met His Phe Asp Ala Gln Pro  
85 90 95

Gln Val Cys Ala Gln Val Val Arg Leu Lys Thr Ile Ala Glu Asp Ile  
100 105 110

Asn Glu Asn Ile Arg Asn Gly Leu Asp Val Ser Ala Leu Pro Ser Phe  
115 120 125

Ala Trp Leu Arg Ala Val Ser Val Arg Asn Pro Leu Ala Lys Gln Thr  
130 135 140

Ile Val Arg Val Asp Phe Glu Thr Leu Pro Thr Pro Gly Thr Pro Pro  
145 150 155 160

Pro	Phe	Pro	Ile	Ala	Ser	Lys	Lys	Phe	Ser	Leu	Thr	Ala	Phe	Ser	Leu	
				165					170					175		
Ser	Phe	Val	Ala	Gln	Ser	Pro	Ser	Asp	Ile	Ser	Thr	Ser	Leu	Ser	His	
			180					185					190			
Ile	Asp	Tyr	Arg	Val	Leu	Ser	Thr	Ile	Ser	Ile	Thr	Glu	Leu	Lys	Gln	
		195					200					205				
Tyr	Val	Lys	Asp	Gly	His	Leu	Arg	Ser	Cys	Pro	Met	Leu	Glu	Arg	Ser	
	210					215					220					
Ile	Ser	Val	Phe	Asn	Asn	Leu	Ser	Asn	Trp	Val	Gln	Cys	Leu	Ile	Leu	
225					230					235					240	
Asn	Lys	Thr	Thr	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Leu	Val	Lys	Phe	Val	
				245					250					255		
His	Val	Ala	Lys	His	Leu	Arg	Lys	Ile	Asn	Asn	Phe	Asn	Thr	Leu	Met	
			260					265					270			
Ser	Val	Val	Gly	Gly	Ile	Thr	His	Ser	Ser	Val	Ala	Arg	Leu	Ala	Lys	
		275					280					285				
Thr	Tyr	Ala	Val	Leu	Ser	Asn	Asp	Ile	Lys	Lys	Glu	Leu	Thr	Gln	Leu	
	290					295					300					
Thr	Asn	Leu	Leu	Ser	Ala	Gln	His	Asn	Phe	Cys	Glu	Tyr	Arg	Lys	Ala	
305					310					315					320	
Leu	Gly	Ala	Cys	Asn	Lys	Lys	Phe	Arg	Ile	Pro	Ile	Ile	Gly	Val	His	
				325					330					335		
Leu	Lys	Asp	Leu	Val	Ala	Ile	Asn	Cys	Ser	Gly	Ala	Asn	Phe	Glu	Lys	
			340					345					350			
Thr	Lys	Cys	Ile	Ser	Ser	Asp	Lys	Leu	Val	Lys	Leu	Ser	Lys	Leu	Leu	
		355					360					365				
Ser	Asn	Phe	Leu	Val	Phe	Asn	Gln	Lys	Gly	His	Asn	Leu	Pro	Glu	Met	
	370					375					380					
Asn	Met	Asp	Leu	Ile	Asn	Thr	Leu	Lys	Val	Ser	Leu	Asp	Ile	Arg	Tyr	
385					390					395					400	
Asn	Asp	Asp	Asp	Ile	Tyr	Glu	Leu	Ser	Leu	Arg	Arg	Glu	Pro	Lys	Thr	
				405					410					415		
Phe	Met	Asn	Phe	Glu	Pro	Ser	Arg	Gly	Leu	Val	Phe	Ala	Glu	Trp	Ala	
			420					425					430			
Ser	Gly	Val	Thr	Val	Ala	Pro	Asp	Asn	Ala	Thr	Val	Ser	Lys	His	Ile	
		435					440					445				
Ser	Ala	Met	Val	Asp	Ala	Val	Phe	Lys	His	Tyr	Asp	His	Asp	Arg	Asp	
	450					455					460					

Gly Phe Ile Ser Gln Glu Glu Phe Gln Leu Ile Ala Gly Asn Phe Pro  
 465 470 475 480  
 Phe Ile Asp Ala Phe Val Asn Ile Asp Val Asp Met Asp Gly Gln Ile  
 485 490 495  
 Ser Lys Asp Glu Leu Lys Thr Tyr Phe Met Ala Ala Asn Lys Asn Thr  
 500 505 510  
 Lys Asp Leu Arg Arg Gly Phe Lys His Asn Phe His Glu Thr Thr Phe  
 515 520 525  
 Leu Thr Pro Thr Thr Cys Asn His Cys Asn Lys Leu Leu Trp Gly Ile  
 530 535 540  
 Leu Arg Gln Gly Phe Lys Cys Lys Asp Cys Gly Leu Ala Val His Ser  
 545 550 555 560  
 Cys Cys Lys Ser Asn Ala Val Ala Glu Cys Arg Arg Lys Ser Ser Ser  
 565 570 575  
 Asn Leu Thr Arg Ala Ala Glu Trp Phe Ala Ser Pro Arg Gly Ser Met  
 580 585 590  
 Arg Ser Arg Ile Ile Asn Thr Cys Asn Asn Ser Gly Ser Thr Pro Asp  
 595 600 605  
 Glu Glu Ile Gly Leu Val Ser Leu Ala Cys Glu Glu Val Phe Glu Asp  
 610 615 620  
 Asp Asp Leu  
 625

<210> 78  
 <211> 530  
 <212> DNA  
 <213> Mus musculus

<400> 78  
 gggatcagag gctgagctgg ttcaagtga cagaaaggctc tgggaggtga actgcattcg 60  
 ggtttgcatt ctgaagtaaa ggacttgggg gtacgaatcg agcactgtgg gaggctctga 120  
 gagggttaact tgggtcttag cccacctggc accggcagcc atggcgagca ctctggacct 180  
 ggacaagggg tgcccgtgga ggagctgctc cgtggctgta tcgaagcett tgatgactct 240  
 ggaaaggtgc gagatccaca gctagtgcgc atgtttctca tgatgcaccc ctggtacata 300  
 ccttcctctc agctggcttc gaaactgctc cacttctatc agcaatcccg gaaggacaac 360  
 tccaattctc tacagatgaa aacgtgtcac ttggtcaggt actggatctc agccttccca 420  
 gcagagttcg acttgaaccc agagctgggt gaacagatca aggagctgaa ggctctgtta 480

gaccaagaag ggaaccgcag gcacagcagc ctcatcgaca tcgagagtgt 530

<210> 79  
 <211> 720  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (90)..(719)

<400> 79  
 cacgcctcgg aaggagggtt tggggtcggt ggtttcacag tgagtgtgtc tgaagccaaa 60

tggtcggaaa ccgttaccgc ctctcctag gcc cgg cta gtg ggg acc cca acc 113

Ala Arg Leu Val Gly Thr Pro Thr  
 1 5

gcc tgc ggc tgc ccc tcc caa gtt cct ccc tgt tgg cca ggc atc cag 161

Ala Cys Gly Cys Pro Ser Gln Val Pro Pro Cys Trp Pro Gly Ile Gln  
 10 15 20

gtc tcc agt ctc cga gct gcg gag aac cca ccg cca cat gcg gct gcc 209

Val Ser Ser Leu Arg Ala Ala Glu Asn Pro Pro Pro His Ala Ala Ala  
 25 30 35 40

cct ttc cat tcg acc ctg tgg gga gcc agg ctt ccg ggg ccc cgt tcc 257

Pro Phe His Ser Thr Leu Trp Gly Ala Arg Leu Pro Gly Pro Arg Ser  
 45 50 55

tcc tgt gtg aac tgg gcc ccc cgc ccc cat tcc cag aca tca agg ccg 305

Ser Cys Val Asn Trp Ala Pro Arg Pro His Ser Gln Thr Ser Arg Pro  
 60 65 70

cgt ctc cag ata gcc acg att tca ttc ctc gct ccc cac agg tcc ctc 353

Arg Leu Gln Ile Ala Thr Ile Ser Phe Leu Ala Pro His Arg Ser Leu  
 75 80 85

tcc cca aaa tat tcc cat ctt gtc cta gcc cat ccc cca gac tat ctc 401

Ser Pro Lys Tyr Ser His Leu Val Leu Ala His Pro Pro Asp Tyr Leu  
 90 95 100

aag gac cag ctg tcc cca cgc ccc cga cct cca cta ggc ctg tgc cac 449

Lys Asp Gln Leu Ser Pro Arg Pro Arg Pro Pro Leu Gly Leu Cys His  
 105 110 115 120

ccg ctg cct gca gga aga cgc ccg gtc ccg ggc cgg gtt agc ccc atg 497  
 Pro Leu Pro Ala Gly Arg Arg Pro Val Pro Gly Arg Val Ser Pro Met  
                   125                  130                  135  
 gga acg cag cgc ctg tgt ggc cgc ggg act caa ggc tgg cct ggc tca 545  
 Gly Thr Gln Arg Leu Cys Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser  
                   140                  145                  150  
 agt gaa cag cac gtc cag gag gcg acc tcg tcc gcg ggt ttg cat tct 593  
 Ser Glu Gln His Val Gln Glu Ala Thr Ser Ser Ala Gly Leu His Ser  
                   155                  160                  165  
 ggg gtg gac gag ctg ggg gtt cgg tcc gag ccc ggt ggg agg ctc ccg 641  
 Gly Val Asp Glu Leu Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro  
                   170                  175                  180  
 gag cgc agc ctg ggc cca gcc cac ccc gcg ccg gcg gcc atg gca ggc 689  
 Glu Arg Ser Leu Gly Pro Ala His Pro Ala Pro Ala Ala Met Ala Gly  
 185                  190                  195                  200  
 acc ctg gac ctg gac aag ggc tgc acg gtg g 720  
 Thr Leu Asp Leu Asp Lys Gly Cys Thr Val  
                   205                  210

<210> 80  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
 Ala Arg Leu Val Gly Thr Pro Thr Ala Cys Gly Cys Pro Ser Gln Val  
   1                  5                  10                  15  
 Pro Pro Cys Trp Pro Gly Ile Gln Val Ser Ser Leu Arg Ala Ala Glu  
                   20                  25                  30  
 Asn Pro Pro Pro His Ala Ala Ala Pro Phe His Ser Thr Leu Trp Gly  
                   35                  40                  45  
 Ala Arg Leu Pro Gly Pro Arg Ser Ser Cys Val Asn Trp Ala Pro Arg  
   50                  55                  60  
 Pro His Ser Gln Thr Ser Arg Pro Arg Leu Gln Ile Ala Thr Ile Ser  
   65                  70                  75                  80  
 Phe Leu Ala Pro His Arg Ser Leu Ser Pro Lys Tyr Ser His Leu Val  
                   85                  90                  95

Leu Ala His Pro Pro Asp Tyr Leu Lys Asp Gln Leu Ser Pro Arg Pro  
                     100                    105                    110  
 Arg Pro Pro Leu Gly Leu Cys His Pro Leu Pro Ala Gly Arg Arg Pro  
                     115                    120                    125  
 Val Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu Cys Gly Arg  
                     130                    135                    140  
 Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val Gln Glu Ala  
                     145                    150                    155                    160  
 Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp Glu Leu Gly Val Arg  
                     165                    170                    175  
 Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly Pro Ala His  
                     180                    185                    190  
 Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys  
                     195                    200                    205  
 Thr Val  
                     210

<210> 81  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 81  
 Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu Glu Val  
           1                    5                    10                    15  
 Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp  
                     20                    25                    30  
 Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val Glu Leu Ser Glu Ala  
                     35                    40                    45  
 Tyr Arg Val Leu Ser Arg Glu Ser Arg Arg Ser Tyr Asp  
                     50                    55                    60

<210> 82  
 <211> 62  
 <212> PRT  
 <213> C. elegans

<400> 82  
 Tyr Tyr Glu Ile Leu Gly Val Ser Lys Thr Ala Glu Glu Arg Glu Ile  
           1                    5                    10                    15

Arg Lys Ala Tyr Lys Arg Leu Ala Met Lys Tyr His Pro Asp Arg Asn  
20 25 30

Gln Gly Asp Lys Glu Ala Glu Ala Lys Phe Lys Glu Ile Lys Glu Ala  
35 40 45

Tyr Glu Val Leu Thr Asp Ser Gln Lys Arg Ala Ala Tyr Asp  
50 55 60

<210> 83  
<211> 37  
<212> PRT  
<213> Homo sapiens

<400> 83  
Gln Arg Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro  
1 5 10 15

Gly Ala Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys  
20 25 30

Glu Leu His Pro Asp  
35

<210> 84  
<211> 37  
<212> PRT  
<213> C. elegans

<400> 84  
Lys Lys Ile Arg Gln Arg Thr His Tyr Glu Val Leu Gly Val Glu Ser  
1 5 10 15

Thr Ala Thr Leu Ser Glu Ile Lys Ser Ala Phe Tyr Ala Gln Ser Lys  
20 25 30

Lys Val His Pro Asp  
35

<210> 85  
<211> 32  
<212> PRT  
<213> Homo sapiens

<400> 85  
Ser Leu His Ser Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu  
1 5 10 15

Ser Arg Glu Gln Ser Arg Arg Ser Tyr Asp Asp Gln Leu Arg Ser Gly  
20 25 30

<210> 86  
 <211> 32  
 <212> PRT  
 <213> C. elegans

<400> 86  
 Ser Ala Thr Ala Ser Phe Leu Glu Leu Lys Asn Ala Tyr Asp Val Leu  
           1                  5                  10                  15  
 Arg Arg Pro Ala Asp Arg Arg Leu Tyr Asp Tyr Gln Leu Arg Gly Gly  
                   20                  25                  30

<210> 87  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 87  
 Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile Ala Phe Arg Lys  
           1                  5                  10                  15  
 Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile Ile  
                   20                  25                  30  
 Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg  
           35                  40

<210> 88  
 <211> 42  
 <212> PRT  
 <213> C. elegans

<400> 88  
 Leu Val Leu Val Ala Gly Tyr Asn Gly Gly Tyr Leu Tyr Leu Leu Ala  
           1                  5                  10                  15  
 Tyr Asn Gln Lys Gln Leu Asp Lys Leu Ile Asp Glu Asp Glu Ile Ala  
                   20                  25                  30  
 Lys Cys Phe Leu Arg Gln Lys Glu Phe Arg  
           35                  40

<210> 89  
 <211> 41  
 <212> PRT  
 <213> Homo sapiens

<400> 89  
 Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu Glu Val  
           1                  5                  10                  15



Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp  
20 25 30

Pro Gly Asn Pro Ser Leu His Ser Arg  
35 40

<210> 90  
<211> 41  
<212> PRT  
<213> C. elegans

<400> 90  
Tyr Tyr Glu Ile Ile Gly Val Ser Ala Ser Ala Thr Arg Gln Glu Ile  
1 5 10 15

Arg Asp Ala Phe Leu Lys Lys Thr Lys Gln Leu His Pro Asp Gln Ser  
20 25 30

Arg Lys Ser Ser Lys Ser Asp Ser Arg  
35 40

<210> 91  
<211> 22  
<212> PRT  
<213> Homo sapiens

<400> 91  
Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln  
1 5 10 15

Ser Arg Arg Ser Tyr Asp  
20

<210> 92  
<211> 22  
<212> PRT  
<213> C. elegans

<400> 92  
Gln Phe Met Leu Val Lys Glu Ala Tyr Asp Val Leu Arg Asn Glu Glu  
1 5 10 15

Lys Arg Lys Glu Tyr Asp  
20

<210> 93  
<211> 44  
<212> PRT  
<213> Homo sapiens

<400> 93

Gln Gly Pro Gln Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val  
 1 5 10 15

Leu Gly Tyr Cys Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr  
 20 25 30

Ile Ala Phe Arg Lys Val Lys Gln Met His Leu Asn  
 35 40

<210> 94  
 <211> 44  
 <212> PRT  
 <213> C. elegans

<400> 94

Arg Asn Pro Glu Asp Glu Tyr Leu Arg Glu Lys Trp Lys Asn Arg Met  
 1 5 10 15

Leu Val Val Leu Ala Ala Thr Val Met Ala Leu Ile Gly Ala Asn Ile  
 20 25 30

Val Tyr Ile Arg Lys Leu Gln Ala Asp Arg Leu Ser  
 35 40

<210> 95  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<400> 95

Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu Glu Val  
 1 5 10 15

Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp  
 20 25 30

Pro Gly Asn Pro  
 35

<210> 96  
 <211> 36  
 <212> PRT  
 <213> S. pombe

<400> 96

Tyr Tyr Asp Leu Leu Gly Ile Ser Thr Asp Ala Thr Ala Val Asp Ile  
 1 5 10 15

Lys Lys Ala Tyr Arg Lys Leu Ala Val Lys Tyr His Pro Asp Lys Asn  
 20 25 30

Pro Asp Asp Pro  
35

<210> 97  
<211> 40  
<212> PRT  
<213> Homo sapiens

<400> 97  
Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln  
1 5 10 15  
Ser Arg Arg Ser Tyr Asp Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys  
20 25 30  
Ser Pro Arg Thr Thr Val His Asp  
35 40

<210> 98  
<211> 40  
<212> PRT  
<213> S. pombe

<400> 98  
Lys Phe Gln Lys Ile Ser Glu Ala Tyr Gln Val Leu Gly Asp Glu Lys  
1 5 10 15  
Leu Arg Ser Gln Tyr Asp Gln Phe Gly Lys Glu Lys Ala Val Pro Glu  
20 25 30  
Gln Gly Phe Thr Asp Ala Tyr Asp  
35 40

<210> 99  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 99  
Asp Arg Ile Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg  
1 5 10 15  
Ala Asn Arg Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu  
20 25

<210> 100  
<211> 29  
<212> PRT  
<213> S. pombe

<400> 100

Asp Arg Lys Lys Asn Ala Gln Ile Arg Glu Arg Glu Ala Leu Ala Lys  
1 5 10 15

Arg Glu Gln Glu Met Ile Glu Asp Arg Arg Gln Arg Ile  
20 25

<210> 101  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 101  
Pro Gln Gly Pro Gln Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln  
1 5 10 15

Val Leu Gly

<210> 102  
<211> 19  
<212> PRT  
<213> S. pombe

<400> 102  
Pro Gln Gly Ala Ser Glu Lys Phe Gln Lys Ile Ser Glu Ala Tyr Gln  
1 5 10 15

Val Leu Gly

<210> 103  
<211> 71  
<212> PRT  
<213> Homo sapiens

<400> 103  
Ala Gly Gln Arg Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val  
1 5 10 15

His Pro Gly Ala Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys  
20 25 30

Ser Lys Glu Leu His Pro Asp Arg Asp Pro Gly Asn Pro Ser Leu His  
35 40 45

Ser Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu  
50 55 60

Gln Ser Arg Arg Ser Tyr Asp  
65 70

<210> 104

<211> 71  
 <212> PRT  
 <213> *Drosophila virilis*

<400> 104

Ser	Ser	Ser	Arg	Met	Gln	Ala	Lys	Asp	Tyr	Tyr	Ala	Thr	Leu	Gly	Val
1				5					10					15	
Ala	Lys	Asn	Ala	Asn	Ala	Lys	Asp	Ile	Lys	Lys	Ala	Tyr	Tyr	Glu	Leu
		20						25					30		
Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	Pro	Asp	Ala	Ser
		35					40					45			
Lys	Lys	Phe	Gln	Asp	Val	Ser	Glu	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Asp
	50					55					60				
Gln	Lys	Arg	Arg	Glu	Tyr	Asp									
65					70										

<210> 105  
 <211> 397  
 <212> PRT  
 <213> *Homo sapiens*

<400> 105

Met	Val	Lys	Glu	Thr	Thr	Tyr	Tyr	Asp	Val	Leu	Gly	Val	Lys	Pro	Asn
1				5					10					15	
Ala	Thr	Gln	Glu	Glu	Leu	Lys	Lys	Ala	Tyr	Arg	Lys	Leu	Ala	Leu	Lys
		20						25					30		
Tyr	His	Pro	Asp	Lys	Asn	Pro	Asn	Glu	Gly	Glu	Lys	Phe	Lys	Gln	Ile
		35					40					45			
Ser	Gln	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Ala	Lys	Lys	Arg	Glu	Leu	Tyr
	50					55					60				
Asp	Lys	Gly	Gly	Glu	Gln	Ala	Ile	Lys	Glu	Gly	Gly	Ala	Gly	Gly	Gly
65					70					75				80	
Phe	Gly	Ser	Pro	Met	Asp	Ile	Phe	Asp	Met	Phe	Phe	Gly	Gly	Gly	Gly
				85					90					95	
Arg	Met	Gln	Arg	Glu	Arg	Arg	Gly	Lys	Asn	Val	Val	His	Gln	Leu	Ser
		100						105					110		
Val	Thr	Leu	Glu	Asp	Leu	Tyr	Asn	Gly	Ala	Thr	Arg	Lys	Leu	Ala	Leu
		115					120					125			
Gln	Lys	Asn	Val	Ile	Cys	Asp	Lys	Cys	Glu	Gly	Arg	Gly	Gly	Lys	Lys
	130					135					140				
Gly	Ala	Val	Glu	Cys	Cys	Pro	Asn	Cys	Arg	Gly	Thr	Gly	Met	Gln	Ile
145					150					155					160

Arg Ile His Gln Ile Gly Pro Gly Met Val Gln Gln Ile Gln Ser Val  
 165 170 175  
 Cys Met Glu Cys Gln Gly His Gly Glu Arg Ile Ser Pro Lys Asp Arg  
 180 185 190  
 Cys Lys Ser Cys Asn Gly Arg Lys Ile Val Arg Glu Lys Lys Ile Leu  
 195 200 205  
 Glu Val His Ile Asp Lys Gly Met Lys Asp Gly Gln Lys Ile Thr Phe  
 210 215 220  
 His Gly Glu Gly Asp Gln Glu Pro Gly Leu Glu Pro Gly Asp Ile Ile  
 225 230 235 240  
 Ile Val Leu Asp Gln Lys Asp His Ala Val Phe Thr Arg Arg Gly Glu  
 245 250 255  
 Asp Leu Phe Met Cys Met Asp Ile Gln Leu Val Glu Ala Leu Cys Gly  
 260 265 270  
 Phe Gln Lys Pro Ile Ser Thr Leu Asp Asn Arg Thr Ile Val Ile Thr  
 275 280 285  
 Ser His Pro Gly Gln Ile Val Lys His Gly Asp Ile Lys Cys Val Leu  
 290 295 300  
 Asn Glu Gly Met Pro Ile Tyr Arg Arg Pro Tyr Glu Lys Gly Arg Leu  
 305 310 315 320  
 Ile Ile Glu Phe Lys Val Asn Phe Pro Glu Asn Gly Phe Leu Ser Pro  
 325 330 335  
 Asp Lys Leu Ser Leu Leu Glu Lys Leu Leu Pro Glu Arg Lys Glu Val  
 340 345 350  
 Glu Glu Thr Asp Glu Met Asp Gln Val Glu Leu Val Asp Phe Asp Pro  
 355 360 365  
 Asn Gln Glu Arg Arg Arg His Tyr Asn Gly Glu Ala Tyr Glu Asp Asp  
 370 375 380  
 Glu His His Pro Arg Gly Gly Val Gln Cys Gln Thr Ser  
 385 390 395

<210> 106

<211> 340

<212> PRT

<213> Homo sapiens

<400> 106

Met Gly Lys Asp Tyr Tyr Gln Thr Leu Gly Leu Ala Arg Gly Ala Ser  
 1 5 10 15

Asp Glu Glu Ile Lys Arg Ala Tyr Arg Arg Gln Ala Leu Arg Tyr His  
                     20                    25                    30  
 Pro Asp Lys Asn Lys Glu Pro Gly Ala Glu Glu Lys Phe Lys Glu Ile  
                     35                    40                    45  
 Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Arg Lys Arg Glu Ile Phe  
                     50                    55                    60  
 Asp Arg Tyr Gly Glu Glu Gly Leu Lys Gly Ser Gly Pro Ser Gly Gly  
                     65                    70                    75                    80  
 Ser Gly Gly Gly Ala Asn Gly Thr Ser Phe Ser Tyr Thr Phe His Gly  
                     85                    90                    95  
 Asp Pro His Ala Met Phe Ala Glu Phe Phe Gly Gly Arg Asn Pro Phe  
                     100                    105                    110  
 Asp Thr Phe Phe Gly Gln Arg Asn Gly Glu Glu Gly Met Asp Ile Asp  
                     115                    120                    125  
 Asp Pro Phe Ser Gly Phe Pro Met Gly Met Gly Gly Phe Thr Asn Val  
                     130                    135                    140  
 Asn Phe Gly Arg Ser Arg Ser Ala Gln Glu Pro Ala Arg Lys Lys Gln  
                     145                    150                    155                    160  
 Asp Pro Pro Val Thr His Asp Leu Arg Val Ser Leu Glu Glu Ile Tyr  
                     165                    170                    175  
 Ser Gly Cys Thr Lys Lys Met Lys Ile Ser His Lys Arg Leu Asn Pro  
                     180                    185                    190  
 Asp Gly Lys Ser Ile Arg Asn Glu Asp Lys Ile Leu Thr Ile Glu Val  
                     195                    200                    205  
 Lys Lys Gly Trp Lys Glu Gly Thr Lys Ile Thr Phe Pro Lys Glu Gly  
                     210                    215                    220  
 Asp Gln Thr Ser Asn Asn Ile Pro Ala Asp Ile Val Phe Val Leu Lys  
                     225                    230                    235                    240  
 Asp Lys Pro His Asn Ile Phe Lys Arg Asp Gly Ser Asp Val Ile Tyr  
                     245                    250                    255  
 Pro Ala Arg Ile Ser Leu Arg Glu Ala Leu Cys Gly Cys Thr Val Asn  
                     260                    265                    270  
 Val Pro Thr Leu Asp Gly Arg Thr Ile Pro Val Val Phe Lys Asp Val  
                     275                    280                    285  
 Ile Arg Pro Gly Met Arg Arg Lys Val Pro Gly Glu Gly Leu Pro Leu  
                     290                    295                    300

Pro Lys Thr Pro Glu Lys Arg Gly Asp Leu Ile Ile Glu Phe Glu Val  
305 310 315 320

Ile Phe Pro Glu Arg Ile Pro Gln Thr Ser Arg Thr Val Leu Glu Gln  
325 330 335

Val Leu Pro Ile  
340

<210> 107

<211> 351

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Tyr Tyr Glu Ile Leu Asp Val Pro Arg Ser Ala Ser Ala  
1 5 10 15

Asp Asp Ile Lys Lys Ala Tyr Arg Arg Lys Ala Leu Gln Trp His Pro  
20 25 30

Asp Lys Asn Pro Asp Asn Lys Glu Phe Ala Glu Lys Lys Phe Lys Glu  
35 40 45

Val Ala Glu Ala Tyr Glu Val Leu Ser Asp Lys His Lys Arg Glu Ile  
50 55 60

Tyr Asp Arg Tyr Gly Arg Glu Gly Leu Thr Gly Thr Gly Thr Gly Pro  
65 70 75 80

Ser Arg Ala Glu Ala Gly Ser Gly Gly Pro Gly Phe Thr Phe Thr Phe  
85 90 95

Arg Ser Pro Glu Glu Val Phe Arg Glu Phe Phe Gly Ser Gly Asp Pro  
100 105 110

Phe Ala Glu Leu Phe Asp Asp Leu Gly Pro Phe Ser Glu Leu Gln Asn  
115 120 125

Arg Gly Ser Arg His Ser Gly Pro Phe Phe Thr Phe Ser Ser Ser Phe  
130 135 140

Pro Gly His Ser Asp Phe Ser Ser Ser Ser Phe Ser Phe Ser Pro Gly  
145 150 155 160

Ala Gly Ala Phe Arg Ser Val Ser Thr Ser Thr Thr Phe Val Gln Gly  
165 170 175

Arg Arg Ile Thr Thr Arg Arg Ile Met Glu Asn Gly Gln Glu Arg Val  
180 185 190

Glu Val Glu Glu Asp Gly Gln Leu Lys Ser Val Thr Ile Asn Gly Val  
195 200 205



Pro Asp Asp Leu Ala Arg Gly Leu Glu Leu Ser Arg Arg Glu Gln Gln  
 210 215 220  
 Pro Ser Val Thr Ser Arg Ser Gly Gly Thr Gln Val Gln Gln Thr Pro  
 225 230 235 240  
 Ala Ser Cys Pro Leu Asp Ser Asp Leu Ser Glu Asp Glu Asp Leu Gln  
 245 250 255  
 Leu Ala Met Ala Tyr Ser Leu Ser Glu Met Glu Ala Ala Gly Lys Lys  
 260 265 270  
 Pro Ala Gly Gly Arg Glu Ala Gln His Arg Arg Gln Gly Arg Pro Arg  
 275 280 285  
 Pro Ser Thr Lys Ile Gln Ala Trp Gly Gly Pro Arg Arg Val Arg Gly  
 290 295 300  
 Val Lys Gln Pro Asn Ala Val His Pro Gln Arg Arg Arg Pro Leu Ala  
 305 310 315 320  
 Ala Ser Ser Ser Glu His Arg Ala Gln Pro Asp Leu Ile Gln Ile Leu  
 325 330 335  
 Thr Gly Gly Ser Asp Ser Leu Trp Glu Glu Lys Arg Gly Val Ser  
 340 345 350

<210> 108  
 <211> 848  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (30)..(764)

<400> 108  
 caaggagcct ctgcctgccc gtcgtcgtc atg ccg tcc ctg ttg ctc cag ctg 53  
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 1 5  
 ccc ctg cgc cta tgc cgg ctg tgg ccg cat agc ctt tcc atc cga ctt 101  
 Pro Leu Arg Leu Cys Arg Leu Trp Pro His Ser Leu Ser Ile Arg Leu  
 10 15 20  
 ctc aca gcc gcc aca ggg cag cgg tct gtc cct act aat tac tat gaa 149  
 Leu Thr Ala Ala Thr Gly Gln Arg Ser Val Pro Thr Asn Tyr Tyr Glu  
 25 30 35 40  
 ttg ttg ggc gtg cat ccg ggt gcc agc gct gaa gag att aaa cgt gct 197

Leu	Leu	Gly	Val	His	Pro	Gly	Ala	Ser	Ala	Glu	Glu	Ile	Lys	Arg	Ala		
				45					50					55			
ttt	ttc	acc	aag	tca	aaa	gag	cta	cac	cct	gat	cga	gac	cct	ggg	aac	245	
Phe	Phe	Thr	Lys	Ser	Lys	Glu	Leu	His	Pro	Asp	Arg	Asp	Pro	Gly	Asn		
			60					65					70				
cca	gcc	ctg	cat	agc	cgc	ttt	gtg	gag	ctg	aat	gag	gca	tat	cga	gtg	293	
Pro	Ala	Leu	His	Ser	Arg	Phe	Val	Glu	Leu	Asn	Glu	Ala	Tyr	Arg	Val		
		75					80					85					
ctc	agt	cgt	gag	gaa	agt	cgt	cgt	aac	tat	gac	cac	cag	ctg	cat	tca	341	
Leu	Ser	Arg	Glu	Glu	Ser	Arg	Arg	Asn	Tyr	Asp	His	Gln	Leu	His	Ser		
	90					95					100						
gcc	agt	cct	cca	aag	tct	tca	ggg	agc	aca	gcc	gag	cct	aag	tat	acg	389	
Ala	Ser	Pro	Pro	Lys	Ser	Ser	Gly	Ser	Thr	Ala	Glu	Pro	Lys	Tyr	Thr		
105					110					115					120		
caa	cag	aca	cac	agc	agc	tcc	tgg	gaa	ccc	ccc	aac	gct	caa	tac	tgg	437	
Gln	Gln	Thr	His	Ser	Ser	Ser	Trp	Glu	Pro	Pro	Asn	Ala	Gln	Tyr	Trp		
				125					130					135			
gcc	cag	ttc	cac	agt	gtg	agg	ccg	cag	ggg	ccg	gag	tca	agg	aag	cag	485	
Ala	Gln	Phe	His	Ser	Val	Arg	Pro	Gln	Gly	Pro	Glu	Ser	Arg	Lys	Gln		
			140					145					150				
cag	cgt	aaa	cac	aac	cag	cgg	gtc	ctg	ggg	tac	tgc	ctc	ctg	ctc	atg	533	
Gln	Arg	Lys	His	Asn	Gln	Arg	Val	Leu	Gly	Tyr	Cys	Leu	Leu	Leu	Met		
		155					160					165					
gtg	gca	ggc	atg	ggc	ctg	cac	tat	gtt	gcc	ttc	agg	aag	ctg	gag	cag	581	
Val	Ala	Gly	Met	Gly	Leu	His	Tyr	Val	Ala	Phe	Arg	Lys	Leu	Glu	Gln		
	170					175					180						
gtg	cat	cgc	agc	ttc	atg	gat	gaa	aag	gac	cgg	atc	att	aca	gcc	atc	629	
Val	His	Arg	Ser	Phe	Met	Asp	Glu	Lys	Asp	Arg	Ile	Ile	Thr	Ala	Ile		
185					190					195					200		
tac	aat	gac	act	cgg	gcc	agg	gcc	agg	gcc	aac	aga	gcc	agg	att	cag	677	
Tyr	Asn	Asp	Thr	Arg	Ala	Arg	Ala	Arg	Ala	Asn	Arg	Ala	Arg	Ile	Gln		
				205					210					215			
cag	gag	cgc	cac	gag	agg	cag	cag	cct	cgg	gca	gaa	ccc	tcc	ctg	cct	725	

Gln Glu Arg His Glu Arg Gln Gln Pro Arg Ala Glu Pro Ser Leu Pro  
220 225 230  
cca gaa agc tcc agg atc atg ccc cag gac aca agc ccc tgagaggctt 774  
Pro Glu Ser Ser Arg Ile Met Pro Gln Asp Thr Ser Pro  
235 240 245  
aactaaatgg gaccttcatt ggtcctctcc ctgctgctg tccagaacta cacgtgcaat 834  
aaactcattt tcag 848

<210> 109  
<211> 245  
<212> PRT  
<213> Mus musculus

<400> 109  
Met Pro Ser Leu Leu Leu Gln Leu Pro Leu Arg Leu Cys Arg Leu Trp  
1 5 10 15  
Pro His Ser Leu Ser Ile Arg Leu Leu Thr Ala Ala Thr Gly Gln Arg  
20 25 30  
Ser Val Pro Thr Asn Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala  
35 40 45  
Ser Ala Glu Glu Ile Lys Arg Ala Phe Phe Thr Lys Ser Lys Glu Leu  
50 55 60  
His Pro Asp Arg Asp Pro Gly Asn Pro Ala Leu His Ser Arg Phe Val  
65 70 75 80  
Glu Leu Asn Glu Ala Tyr Arg Val Leu Ser Arg Glu Glu Ser Arg Arg  
85 90 95  
Asn Tyr Asp His Gln Leu His Ser Ala Ser Pro Pro Lys Ser Ser Gly  
100 105 110  
Ser Thr Ala Glu Pro Lys Tyr Thr Gln Gln Thr His Ser Ser Ser Trp  
115 120 125  
Glu Pro Pro Asn Ala Gln Tyr Trp Ala Gln Phe His Ser Val Arg Pro  
130 135 140  
Gln Gly Pro Glu Ser Arg Lys Gln Gln Arg Lys His Asn Gln Arg Val  
145 150 155 160  
Leu Gly Tyr Cys Leu Leu Leu Met Val Ala Gly Met Gly Leu His Tyr  
165 170 175  
Val Ala Phe Arg Lys Leu Glu Gln Val His Arg Ser Phe Met Asp Glu  
180 185 190

Lys Asp Arg Ile Ile Thr Ala Ile Tyr Asn Asp Thr Arg Ala Arg Ala  
 195 200 205  
 Arg Ala Asn Arg Ala Arg Ile Gln Gln Glu Arg His Glu Arg Gln Gln  
 210 215 220  
 Pro Arg Ala Glu Pro Ser Leu Pro Pro Glu Ser Ser Arg Ile Met Pro  
 225 230 235 240  
 Gln Asp Thr Ser Pro  
 245

<210> 110  
 <211> 120  
 <212> DNA  
 <213> Homo sapiens

<400> 110  
 ttgaagtcta gcccatacct ggtccaatgc gctcttggtta gcctcctttc ccagctgccc 60  
 gcccgccgcc atgccgcct tactgccct gcgcctgtg ccggctgtgg ccccgcaacc 120

<210> 111  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: The amino acid  
 sequence encoded by the nucleotide sequence of SEQ  
 ID NO:20.

<400> 111  
 Glu Phe Gly Thr Ser  
 1 5